

SEQUENCE LISTING

<110> FRANKARD, VALERIE
MIRONOV, VLADIMIR

<120> PLANTS HAVING MODIFIED GROWTH CHARACTERISTICS AND A METHOD FOR
MAKING THE SAME

<130> 4559-061539

<140> 10/580,085

<141> 2007-05-09

<150> PCT/EP2004/053030

<151> 2004-11-19

<150> 60/528,113

<151> 2003-12-09

<150> EP 03104280.7

<151> 2003-11-19

<160> 37

<170> PatentIn version 3.5

<210> 1

<211> 1428

<212> DNA

<213> *Nicotiana tabacum*

<220>

<223> Seedy1 coding sequence (CDS0689)

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ctgaaacccc ttctggttag gccatcagat tcctttgaat ctgatttgtc aagtaaggaa	180
aatcaaacct ctttatttga gaattcatct gttaatctct catctccgtt acccataaag	240
ccacttaacc ctaatggggc tctggaaaat tcaagactca agccgaacaa gcccaattcc	300
aaacagagtc ttgatgagat ggcggtctaga aagagcggaa agggaaatga ttccgtgat	360
gagaagaaaa tagacgagga aattgaagaa attcagatgg agattagtag gttgagttca	420
agattagag ctttgagaat tgaaaaggct gagaaaactg ttgctaagac tgttgaaaag	480
cgaggaaggg ttgtggcagc aaagtattat gagccaaaac aaagtgttat taagattgaa	540
gagcgtatat caatgagtgc aagaacaaag gtggagcaga gaaggggtct tagtttagga	600
ccatctgaga tttttactgg aacgcggcgg cgagggttga gtatggggcc atcagatatt	660
ctagcagga caacaaaggc acggcaattg ggaagcaag agatgattat tactcctatt	720

cagccaatac aaaacaggcg aaagtcgtgt ttttgaagc ttcaagagat tgaagaagag	780
ggaaaaagtt caagccttag tcctaaatca agaaaaactg ctgcaagaac aatggttaca	840
acaaggcagc cagttactac aattgcatca aagaagaatt tgaaaaaaga tgatggactt	900
ttgagttcag ttcagccaaa gaagttgttt aaagatctcg aaaagtctgc tgctgctaatt	960
aagaagcccc agaggccggg gagggttgtg gctagtagtg ataatcagag tacaattcag	1020
tcatcagtag tgagaaagag gtctttacct gaaaatgata aggatgagag taagagaaat	1080
gataagaaac ggtcgttata tgtagggaaa acgcgtgtgt ctcaactga gagcaagaat	1140
ttgggtactg aaagtagggt gaaaaagaga tgggaaattc ctagtggatg tgtagttcat	1200
ggaaacacag agagtggaaa atctccacta agcattattg tgaagcctga tttgcttccg	1260
cgaattagga ttgctcggtg tgtgaatgag actcttaggg attctggacc tgctaaaaga	1320
atgatagagt tgatagccaa gaaatcgttt ttcagtagtg atgaagataa ggagccacct	1380
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<210> 2
 <211> 475
 <212> PRT
 <213> Nicotiana tabacum

<220>
 <223> Seedyl protein (CDS0689)

<400> 2
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Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Leu Ser
 20 25 30

Ser Leu Lys Arg Ser Trp Ser Pro Leu Lys Pro Leu Ser Val Arg Pro
 35 40 45

Ser Asp Ser Phe Glu Ser Asp Leu Ser Ser Lys Glu Asn Gln Thr Pro
 50 55 60

Leu Phe Glu Asn Ser Ser Val Asn Leu Ser Ser Pro Leu Pro Ile Lys
 65 70 75 80

Pro Leu Asn Pro Asn Gly Ala Leu Glu Asn Ser Arg Leu Lys Pro Asn
 85 90 95

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser
100 105 110

Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile
115 120 125

Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala
130 135 140

Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys
145 150 155 160

Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val
165 170 175

Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu
180 185 190

Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr
195 200 205

Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr
210 215 220

Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile
225 230 235 240

Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu
245 250 255

Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys
260 265 270

Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile
275 280 285

Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val
290 295 300

Gln Pro Lys Lys Leu Phe Lys Asp Leu Glu Lys Ser Ala Ala Ala Asn
305 310 315 320

Lys Lys Pro Gln Arg Pro Gly Arg Val Val Ala Ser Arg Tyr Asn Gln
325 330 335

Ser Thr Ile Gln Ser Ser Val Val Arg Lys Arg Ser Leu Pro Glu Asn
 340 345 350

Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val
 355 360 365

Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu
 370 375 380

Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His
 385 390 395 400

Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro
 405 410 415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu
 420 425 430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys
 435 440 445

Ser Phe Phe Ser Ser Asp Glu Asp Lys Glu Pro Pro Val Cys Gln Val
 450 455 460

Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu
 465 470 475

<210> 3
 <211> 1336
 <212> DNA
 <213> *Oryza sativa*

<220>
 <223> Seedyl coding sequence

<400> 3
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 ggcgacaagg agaatcaccg ccccgagggtt gttgatgtcg ccgccggcta cgacgtcgag 180
 gccgagatcg gccacatcga ggcggagatc ctgcgcctct cgtcccggtt ccaccatctc 240
 cgctgttcca agcagccgga gccaaccgc gacgacgctc cgatggggga gatggtcgcg 300
 aaggtgaggc cccggccgag gggcctcagc ctcgggcccc tggatgtgat ctccatcgtc 360

aatcgtgaga agcatccgct gcgcaccaag cagcctccgg cgacgcgggg cagggggctc	420
agcctcgggc ccatggagat cgccgcggcg aacctaggg tgcccgggc ggcgcagcat	480
cagcaacagc aacgcgctgg caccggcgcg atcctgaagc caatcaagga gcctccggtg	540
cagcgtcgca ggggctcag cctcggggcg ttgagatcc accacggcgt cgcgagcaag	600
gcaccagcgg cggcgcgagc caagccgttc accaccaagc tcaacgccat tcgagaagaa	660
accgcacct ccaagcaatt cgccgtcccc gccaaagccat ggccgtcgag caatacaagg	720
cagacactgg actcgaggca aggaacagca gcaagtcgag cgaaggcgag gagcccagc	780
cccaggccca ggaggcaatc caatggcaag gctactgaca caaggggagg caacaagggtg	840
gtgatgagc tcaagcccaa aggtgcgtcg tcaagtcaga gcgcgacgc cgccgcgcc	900
gccactgcca agaggatgg ggggagctcc aagatgagg tcatcccgag ccgctacagc	960
ctcactcctg gcgcttcct tggaagcagt ggagcacagg agaggcgacg caagcagtct	1020
ctccaggat catcagggga tgcaaccag aatgaggaaa tcagagcgaa ggtatcgag	1080
ccttccaat atccactct tctcaaacg atctccaagg ttgctgaaat gctcccaaag	1140
atcaggacca tgccgcctcc tgacgagagc cctgcgatt ccggtgcgc caagcgggtt	1200
gccgaattgg tcgggaagcg ctcgttcttc acgctgcag ccgaggacgg gcgggcgctc	1260
gacgtcgaag caccgcaggc ggtcgcagaa gcttgagatg aaccaccatg gttgatccg	1320
ttccttccat cagctc	1336

<210> 4
 <211> 431
 <212> PRT
 <213> *Oryza sativa*

<220>
 <223> Seedyl protein

<400> 4
 Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala
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Ala Phe Asp Asp Ser Ser Cys Ser Arg Ser Ala Trp Leu Pro Gln Ser
 20 25 30

Pro Ala Val Ala Ala Val Arg Lys Gly Asp Lys Glu Asn His Arg Pro
 35 40 45

Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly

50

55

60

His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu
65 70 75 80

Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly
85 90 95

Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly
100 105 110

Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg
115 120 125

Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro
130 135 140

Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His
145 150 155 160

Gln Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys
165 170 175

Glu Pro Pro Val Gln Arg Arg Arg Gly Val Ser Leu Gly Pro Leu Glu
180 185 190

Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys
195 200 205

Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser
210 215 220

Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg
225 230 235 240

Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala
245 250 255

Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr
260 265 270

Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly
275 280 285

Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Ala Thr Ala Lys
 290 295 300

Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser
 305 310 315 320

Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg
 325 330 335

Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu
 340 345 350

Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro
 355 360 365

Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met
 370 375 380

Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val
 385 390 395 400

Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp
 405 410 415

Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala
 420 425 430

<210> 5
 <211> 1860
 <212> DNA
 <213> Medicago trunculata

<220>
 <223> Seedy1 coding sequence

<400> 5
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 cctatttaca gggatcttaa atataattaa ccctaattat tatgacagaa acccttttga 120
 aatcacatcg gagcgtgtat gtagtgcggt ttacatcca acggccagta agagcgtaac 180
 tttattttctt cctcttcaa tctccaacgg tcacataatc tcttccaaat acaataatt 240
 cctcttttca acctactct tcattttctc aaccctaaacc caaaaaacta atcagattct 300
 tcttaaatct tgaaaccttt ctcccaaaag cacttaata aaaaagcact taacatgaa 360
 taacacaac aacaacaaca ttcttcttca ttccacacag gttcaagtgt ggaacaacgc 420

agcattcgat ggtgaagatt tcgccatgaa ttcatcttct gattccatca aagagaatct	480
aaacccatcc gcattcaaca ttgttccttc ttcaaacaaa agaactattg atgatgaaat	540
tcgggaaatt gaaagtgaaa ttaagcgatt aacttcgaag ctggaattgc ttctgtttga	600
aaaagctgaa agaaaaatcg cttctgaaaa gcgtgttagt ggaattggta ctggaagaat	660
agtagcagcg aagtttatgg aaccgaagaa aaacgttaca ccgaaacgaa acgggtgtcgt	720
tttcaaggag gagacaccga aacgaaacgg tgctgtttcg gatacgccga aatctagggt	780
taattggaga agagggatga gtttaggtcc gatggagatt gccgggaaa tgatggcacc	840
gccggcgatg acgattactc cggcgacggt gaatcggagg aagtcttgtt tctgaaacc	900
gcaggaaagt tgtgaagtaa tgccgtcggg gattactccg gcgacggtga ataggaggaa	960
atcttgtttt ttgaaacctc aagaaagttg tgaagaaaa cgaagaaaa cgatttgcaa	1020
accgaatttg aatttgaatt caaattcagt taattctgcg gttggatcga ttaagcgtgt	1080
gaagaagaaa gatgaagaaa ttgctcaggt tcaaccgaag aagctgtttg aaggtgaaaa	1140
atcagtgaag aaatcgttga aacaaggtag aattgttgca agccggtata attccggtgg	1200
tggtggtggt gatgcgagga aaagatcggt ttccggagaat aataagggtt tagggagtga	1260
aatcagggct aagaagagat gggagatacc aattgaagaa gtgagtgga gtggttttgt	1320
tatgttaccg aagatttcca caatgaggtt tgttgatgag agtcctagag attctggtgc	1380
tgttaaaaga gttgctgaat tgaatggaaa aagatcttac ttttgtgatg aagatgagga	1440
ggagagagtg atggtggagg aagaaggtgg ttctgtttgt cagggtttga attttgctga	1500
agatgatgat gatgatgatg attatggtga acaagggtaa ttgtggaat tggaattgat	1560
ttgtttttgt ggggttgtgt ggaactggct atgttctgct tgattctttt gcattttggt	1620
gtgaaactaa agatgaggtg aaaagtttat gcttgttaaa ttggattggt ttatatgttt	1680
tgaaataata acaacaagca tgtgtcttgc ttaataattg tatattgttt tgtttgtttt	1740
ataatgatat ggatttaatt tgtatacaca atataatata gtatgcattg agagagtttt	1800
tcgttcagta ttcattctga ttttagtggt tatctcattc tagaagattg tattttgttg	1860

<210> 6

<211> 394

<212> PRT

<213> Medicago trunculata

<220>

<223> Seedy1 protein

<400> 6

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Gln Val Trp Asn Asn Ala Ala Phe Asp Gly Glu Asp Phe Ala Met Asn
20 25 30

Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn
35 40 45

Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu
50 55 60

Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg
65 70 75 80

Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly
85 90 95

Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys
100 105 110

Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro
115 120 125

Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp
130 135 140

Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met
145 150 155 160

Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys
165 170 175

Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly
180 185 190

Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro
195 200 205

Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn
210 215 220

Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys
225 230 235 240

Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys
245 250 255

Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg
260 265 270

Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Gly Asp Ala Arg
275 280 285

Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg
290 295 300

Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly
305 310 315 320

Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser
325 330 335

Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys
340 345 350

Arg Ser Tyr Phe Cys Asp Glu Asp Glu Glu Glu Arg Val Met Val Glu
355 360 365

Glu Glu Gly Gly Ser Val Cys Gln Val Leu Asn Phe Ala Glu Asp Asp
370 375 380

Asp Asp Asp Asp Asp Tyr Gly Glu Gln Gly
385 390

<210> 7
<211> 674
<212> DNA
<213> Saccharum sp.

<220>
<223> Seedyl coding sequence (partial 5' end)

<220>
<221> modified_base
<222> (362)..(362)
<223> a, c, t or g

<220>
<221> modified_base
<222> (372)..(372)

<223> a, c, t o r g

<220>

<221> modified base

<222> (674)..(674)

<223> a, c, t o r g

<400> 7

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tccggctcag ggggctctcc ggcggcggtg gcgatggagg aggaccgcgt catcccgtg      180
gtgcacgtct ggaacaacgc cgccttcgac cagcctcct cctccgcgtg gcacgcccac      240
tcccctgtgc ccgcgagcgc acgtcgcgag gcggaggggg acaaggagaa ccaccgcccc      300
gaccccgacc ccgacgtcga ggcggagatc ggccacatcg aggcggagat cctgcgcctg      360
tnctccccgc tncaccacct tcgcacctcc aagcagtcgg agccgtccaa gcgcggagag      420
gtcgcgcccc cgcccgcggc gaaggcgaaa gcggcgcgcg cggcgcggct gcggacgcgg      480
gggtcagccc tgggcccgct cgacgtcgcc gctgccggtg accccaacc gctcaccacc      540
gacaaccagc agcagcagcc gcgtgccgcg cagggtctga agccgatcaa gcaggccacg      600
gcggcgggcg gcaagggcgt aagacttggg ccccttcgac atggtcggcg cgaaccctag      660
ggtccctccg cccn                                     674
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<210> 8

<211> 166

<212> PRT

<213> Saccharum sp.

<220>

<223> Seedy1 protein (partial N term)

<220>

<221> MOD_RES

<222> (70)..(70)

<223> Any amino acid

<400> 8

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Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala
1          5          10          15
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Ala Phe Asp His Ala Ser Ser Ser Ala Trp His Ala His Ser Pro Val
          20          25          30
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```
Pro Ala Ser Ala Arg Arg Glu Ala Glu Gly Asp Lys Glu Asn His Arg
          35          40          45
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Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala
50 55 60

Glu Ile Leu Arg Leu Xaa Ser Arg Leu His His Leu Arg Thr Ser Lys
65 70 75 80

Gln Ser Glu Pro Ser Lys Arg Gly Glu Val Ala Pro Ala Pro Ala Ala
85 90 95

Lys Ala Lys Ala Ala Ala Ala Arg Leu Arg Thr Arg Gly Leu Ser
100 105 110

Leu Gly Pro Leu Asp Val Ala Ala Ala Gly Asn Pro Asn Pro Leu Thr
115 120 125

Thr Asp Asn Gln Gln Gln Gln Pro Arg Ala Ala Gln Gly Leu Lys Pro
130 135 140

Ile Lys Gln Ala Thr Ala Ala Ala Gly Lys Gly Val Arg Leu Gly Pro
145 150 155 160

Leu Arg His Gly Arg Arg
165

<210> 9
<211> 876
<212> DNA
<213> Zea mays

<220>
<223> Seedy1 coding sequence (partial 3' end)

<220>
<221> modified_base
<222> (869)..(869)
<223> a, c, t or g

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caagcagagc caaggcgagg agcggggagca taagccccag caggttcagg aggcagtcca 180
cttccaaggc tgccgagaca agagcgggaa atgccaaagcc tacagaggcg acgaggggag 240
ggagcgaagc ggtcaatcac accagcaatg tagccacgac gaagaggccg gcggggagct 300
ccaaggtcag ggtgtgtccc agccgctaca gcatcccacc tggtcctctc ctagcagctg 360

tgacacaagc caaccgatgc aagcagtcctc tcccaggatc ggctactgag accagagtaa 420
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 tgctcccaag gattagagcc atgccgcctt ctgatgagag cccgcgtgac tcgggatgtg 540
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 ggcggtggcct ctttttgtag tgtgtgctac tacatagtct actgttacat tcatatcata 780
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 aaagagagtg gaagggttcat ctgctgatnc cttggt 876

<210> 10
 <211> 224
 <212> PRT
 <213> Zea mays

<220>
 <223> Seedyl protein (partial C term)

<400> 10
 Thr Arg Pro Ala Val Arg Glu Glu Glu Gly Gln Arg Ser Lys Glu His
 1 5 10 15

Ala Val Pro Ala Arg Pro Trp Pro Ser Ser Asn Ala Arg His Pro Leu
 20 25 30

Asp Ala Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala Arg Ser Gly
 35 40 45

Ser Ile Ser Pro Ser Arg Phe Arg Arg Gln Ser Thr Ser Lys Ala Ala
 50 55 60

Glu Thr Arg Ala Gly Asn Ala Lys Pro Thr Glu Ala Thr Arg Gly Gly
 65 70 75 80

Ser Glu Ala Val Asn His Thr Ser Asn Val Ala Thr Thr Lys Arg Pro
 85 90 95

Ala Gly Ser Ser Lys Val Arg Val Val Pro Ser Arg Tyr Ser Ile Pro
 100 105 110

Pro Gly Ser Ser Leu Ala Ala Val Thr Gln Gly Asn Arg Cys Lys Gln

115

120

125

Ser Leu Pro Gly Ser Ala Thr Glu Thr Arg Val Asn Leu Thr Glu Pro
130 135 140

Pro Asn Asp Glu Leu Ser Pro Glu Glu Leu Ala Lys Val Ala Glu Leu
145 150 155 160

Leu Pro Arg Ile Arg Thr Met Pro Pro Ser Asp Glu Ser Pro Arg Asp
165 170 175

Ser Gly Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe
180 185 190

Phe Thr Ala Ala Gly Asp Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala
195 200 205

Arg Val Val Glu Leu Glu Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu
210 215 220

<210> 11

<211> 1257

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<223> Seedyl coding sequence

<400> 11

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aacgctgcct tcgacgatgg agattctcaa atcacttccg ccatcgaaagc ttcttcttgg	120
tctcacctca acgaatcatt cgattccgat tgtagcaagg agaatcagtt tccgatttcg	180
gtttctcttt cgctccaatc ctgagtcctg atcaccgaag ctccgtcagc aaaatccaag	240
accgtgaaga ccaaatccgc cgcagatcgg agtaaaaaag gagatatga tgcagagatc	300
gaagaagtag agaaggagat cggacgatta tcgacgaaat tggagtcgct ccgattagag	360
aaggcggagc aaaccgcaag aagcattgct atacgtggaa gaatcggtcc ggcgaagttc	420
atggaatcat ctgagaaca agtgaaatc gacgattcgt gttttacagg atcgaaatca	480
agagccactc gtgaggcggt tagtcttggg ccagcggaga tattcaattc cgcgaagaaa	540
tctgaaactg tgactcctct tcaatcagct cagaatcgac gcaagtcctg tttctttaag	600
cttcctggaa tcgaagaagg tcaagtgcg acacgaggta aaggaagaac gagtttgagt	660

ctgagtcgca gatctcgcaa agcgaaaatg acggcagctc agaagcaagc agctacgacg	720
gtgggggtcaa agagagctgt gaagaaagaa gaaggagttc tcttaacaat ccagcctaag	780
aggctattca aagaagatga aaagaatggt tctttaagga aaccattgaa accaggaaga	840
gttggtggcta gtaggtacag tcaaatgggt aaaacgcaga ctggagagaa agatgttagg	900
aaaaggtcgt tgcctgagga tgaagagaaa gagaatcata agaggtcgga gaagagaaga	960
gcttctgatg aaagtaacaa gagtgaaggg agagtgaaga agagatggga gattccaagt	1020
gaagttgatc tgtatagcag tgggtgagaac ggtgacgagt ctctatagt taaggagcta	1080
cctaagatca gaacgcttcg tcgtgtggga gggagccctc gtgattcagg tgctgctaag	1140
agagttgcag aattacaagc caaggatcgt aacttcactt ttgccagct tctgaagttt	1200
gaagaatgaa tgatccgctt atcaatttga gtaaaatcca caactcttgt tgtgggt	1257

<210> 12
 <211> 402
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> Seedyl protein

<400> 12
 Met Thr Ser Ile Glu Ala Thr Glu Thr Leu Asn Ala Pro Pro Lys Leu
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Gln Ile Trp Asn Asn Ala Ala Phe Asp Asp Gly Asp Ser Gln Ile Thr
 20 25 30

Ser Ala Ile Glu Ala Ser Ser Trp Ser His Leu Asn Glu Ser Phe Asp
 35 40 45

Ser Asp Cys Ser Lys Glu Asn Gln Phe Pro Ile Ser Val Ser Ser Ser
 50 55 60

Leu Gln Ser Ser Val Ser Ile Thr Glu Ala Pro Ser Ala Lys Ser Lys
 65 70 75 80

Thr Val Lys Thr Lys Ser Ala Ala Asp Arg Ser Lys Lys Arg Asp Ile
 85 90 95

Asp Ala Glu Ile Glu Glu Val Glu Lys Glu Ile Gly Arg Leu Ser Thr
 100 105 110

Lys Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Thr Ala Arg Ser
 115 120

Ile Ala Ile Arg Gly Arg Ile Val Pro Ala Lys Phe Met Glu Ser Ser
 130 135 140

Gln Lys Gln Val Lys Phe Asp Asp Ser Cys Phe Thr Gly Ser Lys Ser
 145 150 155 160

Arg Ala Thr Arg Arg Gly Val Ser Leu Gly Pro Ala Glu Ile Phe Asn
 165 170 175

Ser Ala Lys Lys Ser Glu Thr Val Thr Pro Leu Gln Ser Ala Gln Asn
 180 185 190

Arg Arg Lys Ser Cys Phe Phe Lys Leu Pro Gly Ile Glu Glu Gly Gln
 195 200 205

Val Thr Thr Arg Gly Lys Gly Arg Thr Ser Leu Ser Leu Ser Pro Arg
 210 215 220

Ser Arg Lys Ala Lys Met Thr Ala Ala Gln Lys Gln Ala Ala Thr Thr
 225 230 235 240

Val Gly Ser Lys Arg Ala Val Lys Lys Glu Glu Gly Val Leu Leu Thr
 245 250 255

Ile Gln Pro Lys Arg Leu Phe Lys Glu Asp Glu Lys Asn Val Ser Leu
 260 265 270

Arg Lys Pro Leu Lys Pro Gly Arg Val Val Ala Ser Arg Tyr Ser Gln
 275 280 285

Met Gly Lys Thr Gln Thr Gly Glu Lys Asp Val Arg Lys Arg Ser Leu
 290 295 300

Pro Glu Asp Glu Glu Lys Glu Asn His Lys Arg Ser Glu Lys Arg Arg
 305 310 315 320

Ala Ser Asp Glu Ser Asn Lys Ser Glu Gly Arg Val Lys Lys Arg Trp
 325 330 335

Glu Ile Pro Ser Glu Val Asp Leu Tyr Ser Ser Gly Glu Asn Gly Asp
 340 345 350

Glu Ser Pro Ile Val Lys Glu Leu Pro Lys Ile Arg Thr Leu Arg Arg
 355 360 365

Val Gly Gly Ser Pro Arg Asp Ser Gly Ala Ala Lys Arg Val Ala Glu
 370 375 380

Leu Gln Ala Lys Asp Arg Asn Phe Thr Phe Cys Gln Leu Leu Lys Phe
 385 390 395 400

Glu Glu

<210> 13

<211> 3074

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 [PRO0090-CDS0689-terminator] expression cassette
 polynucleotide

<400> 13

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ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcattattac	180
aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgtttttatt	240
attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt	300
gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtgtgaa aaattgcaat	360
cottatcaca ttgacacata aagtgagtga tgagtcataa tattattttc ttgctaccc	420
atcatgtata tatgatagcc acaaagttac tttgatgatg atataaaga acatttttag	480
gtgcacctaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt	540
aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa	600
aatcctcadc atccttcacc acaattcaaa tattatagtt gaagcatagt agtaatttaa	660
atcaactagc gatatacaca gtttgtacaa aaaagcaggc tggtagcgtg ccggaattcc	720
cgggatatcg tcgaccacg cgctccgtga cgcgtgggtt ccactacatc aagacatcta	780
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gagtggttta caataccagc aagggtattga ccagcagat gttcagatat ggaacaatgc	900
agcatttgat aatggagatt ctgaagattt gtcttcgctg aaacgttctt ggtctcctct	960

gaaacccctt	tcggttaggc	catcagattc	ctttgaatct	gattttgtcaa	gtaaggaaaa	1020
tcaaactcct	ttatttgaga	attcatctgt	taatctctca	tctccgttac	ccataaagcc	1080
acttaaccct	aatggggctc	tggaaaaatc	aagactcaag	ccgaacaagc	ccaattccaa	1140
acagagtcct	gatgagatgg	cggcctagaaa	gagcggaaaag	ggaatgatt	tccgtgatga	1200
gaagaaaata	gacgaggaaa	ttgaagaaat	tcagatggag	attagtaggt	tgagttcaag	1260
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gcgtatatca	atgagtgcga	gaacaaaagg	ggagcagaga	aggggtctta	gtttaggacc	1440
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gaagccccag	aggccgggga	gggttggtgc	tagtaggtat	aatcagagta	caattcagtc	1860
atcagtagtg	agaaagaggt	ctttacctga	aaatgataag	gatgagagta	agagaaatga	1920
taagaaacgg	tcgttatctg	tagggaaaac	gcgtgtgtct	caaactgaga	gcaagaattt	1980
gggtactgaa	agtaggggtga	aaaagagatg	ggaaattcct	agtgaagattg	tagttcatgg	2040
aaacacagag	agtgagaaat	ctccactaag	cattattgtg	aagcctgatt	tgctccgcg	2100
aattagagatt	gctcgggtg	tgaatgagac	tcttagggat	tctggacctg	ctaaaagaat	2160
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tctgaattac	attgtatgg	acaatatgaa	taaggttttg	tcttccggca	ggtgtgccaa	2460
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cttctagggg	taacagggta	attatatccc	tctagatcac	aagccccggc	ggtcttctac	2640
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acctgaatga acaattgaaa tgaaaagaaa aaaagtactc catctgttcc aaattaaaaat	2760
tcattttaac cttttaatag gtttatatac taattgatat atgttttctg tatatgtcta	2820
atttgttata atccgggagg tcttctaggg ataacagggt aattatatcc ctctagacaa	2880
cacacacaaa ataagagaaa aaacaaataa tattaatttg agaatgaaca aaaggaccat	2940
atcattcatt aactcttctc catccatttc catttcacag ttcgatagcg aaaaccgaat	3000
aaaaaacaca gtaaatatac agcacacaaa atggtacaag aaaaacagtt ttccaatgc	3060
cataatactc gaac	3074

<210> 14
 <211> 668
 <212> DNA
 <213> *Oryza sativa*

<220>
 <223> Prolamin RP6 promoter sequence

<400> 14	
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gttattgtaa agttctacaa agctaattta aaagttattg cattaactta tttcatatta	180
caacaagag tgatcaatga acaatgaaaa ccatatgaca tactataatt ttgtttttat	240
tattgaaatt atataattca aagagaataa atccacatag ccgtaaagtt ctacatgtgg	300
tgcattacca aaatatatat agcttacaaa acatgacaag cttagtttga aaaattgcaa	360
tccttatcac attgacacat aaagtgagtg atgagtcata atattatatt tcttgctacc	420
catcatgtat atatgatagc cacaaagtta ctttgatgat gatatacaag aacattttta	480
ggtgcacctc acagaatata caaataatat gactcaccta gatcataata gagcatcaag	540
taaaactaac actctaaagc aaccgatggg aaagcatcta taaatagaca agcacaatga	600
aaatcctcat catccttcac cacaattcaa atattatagt tgaagcatag tagtagaatc	660
caacaaca	668

<210> 15
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <221> MOD_RES
 <222> (1)..(2)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (3)..(3)
 <223> Val, Leu or His

<220>
 <221> MOD_RES
 <222> (4)..(4)
 <223> Gln or His

<220>
 <221> MOD_RES
 <222> (5)..(5)
 <223> Any amino acid

<220>
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 <222> (7)..(7)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (10)..(10)
 <223> Ala or Pro

<220>
 <221> MOD_RES
 <222> (11)..(11)
 <223> Phe or Cys

<220>
 <223> See specification as filed for detailed description of
 substitutions and preferred embodiments

<400> 15
 Xaa Xaa Xaa Xaa Xaa Trp Xaa Asn Ala Xaa Xaa Asp
 1 5 10

<210> 16
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Motif 2 CORE peptide

<220>
 <221> MOD_RES
 <222> (4)..(5)
 <223> Any amino acid

<400> 16
Lys Glu Asn Xaa Xaa Pro
1 5

<210> 17
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ile, Val or Ala

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Asp or Glu

<220>
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<222> (3)..(3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Ile or Met

<220>
<221> MOD_RES
<222> (6)..(7)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Ile or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Glu or Gln

<220>
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<222> (10)..(10)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (12)..(13)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (16)..(16)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (17)..(17)

<223> Ser, Thr, Leu, Ile or Ala

<220>

<221> MOD_RES

<222> (18)..(18)

<223> Arg or Lys

<220>

<221> MOD_RES

<222> (20)..(21)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (24)..(24)

<223> Leu, Val, Thr or Ile

<220>

<221> MOD_RES

<222> (25)..(25)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (26)..(26)

<223> Lys or Gln

<220>

<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 17

Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Arg Leu Xaa

1

5

10

15

Xaa Xaa Leu Xaa Xaa Leu Arg Xaa Xaa Xaa

20

25

<210> 18

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Arg or Lys

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<222> (5)..(5)
<223> Arg, Ser or Lys

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Thr or Ile

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Met, Leu, Ala or Val

<220>
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<222> (8)..(8)
<223> Pro or Arg

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<222> (9)..(10)
<223> Any amino acid

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<223> Asp, Gln, Thr or Asn

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Glu or Gly

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<222> (13)..(13)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Pro or Leu

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Cys, Pro or Ala

<220>
<221> MOD_RES
<222> (20)..(20)

<223> Ala, Val or Ile

<220>

<221> MOD_RES

<222> (23)..(23)

<223> Val, Gln, Asn or Ile

<220>

<221> MOD_RES

<222> (24)..(24)

<223> Ala or Ile

<220>

<221> MOD_RES

<222> (25)..(25)

<223> Asp or Glu

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<221> MOD_RES

<222> (26)..(26)

<223> Leu or Arg

<220>

<221> MOD_RES

<222> (27)..(27)

<223> Val, Gln, Asn or Ile

<220>

<221> MOD_RES

<222> (28)..(28)

<223> Gly or Ala

<220>

<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 18

Leu Pro Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Asp
1 5 10 15

Ser Gly Xaa Xaa Lys Arg Xaa Xaa Xaa Xaa Xaa Lys
 20 25

<210> 19

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 19

His His His His His His
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<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 20
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25

<210> 21
<211> 81
<212> PRT
<213> Arabidopsis thaliana

<400> 21
Met Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Thr Asn
1 5 10 15

Ala Ala Phe Asp Ser Ser Ser Ser Ser Ser Ala Trp His Ala His Ala
20 25 30

Thr Pro Val Arg Arg Gly Glu Lys Glu Asn Arg Arg Pro Ala Glu Thr
35 40 45

Asn Asp Ala Asp Ala Glu Ile Ala Arg Ile Glu Ala Glu Ile Leu Arg
50 55 60

Leu Ser Ser Arg Leu His His Leu Arg Val Ser Lys Gly His Asp Ala
65 70 75 80

Lys

<210> 22
<211> 84
<212> PRT
<213> Zea mays

<400> 22
Met Glu Glu Asp Pro Leu Ile Gln Leu Val His Val Trp Ser Asn Ala
1 5 10 15

Ala Cys Asp Asn Ala Ala Ala Ser Ser Ser Val Cys His Ala His Ser
20 25 30

Pro Ala Pro Ala Ser Ala Arg Glu Gly Glu Gly Asp Lys Glu Asn Leu
35 40 45

Arg Arg Glu Pro Asp Val Glu Glu Glu Met Arg His Ile Glu Ala Glu
50 55 60

Ile Leu Arg Leu Ser Leu Arg Leu His His Leu Arg Thr Ser Gln Gln
65 70 75 80

Leu Gln Pro Pro

<210> 23
<211> 85
<212> PRT
<213> Saccharum sp.

<400> 23
Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala
1 5 10 15

Pro Phe Asp His Ala Ser Tyr Ser Ala Trp His Ala His Ser Pro Ala
20 25 30

Arg Ala Ser Ala Gly His Glu Ala Glu Gly Asp Lys Glu Asn His Arg
35 40 45

Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala
50 55 60

Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu Arg Thr Ser Lys
65 70 75 80

Gln Ser Glu Pro Pro
85

<210> 24
<211> 125
<212> PRT
<213> Brassica napus

<400> 24
Met Thr Ser Thr Glu His Thr Glu Thr Leu Asn Ala Pro Glu Leu Gln
1 5 10 15

Ile Trp Asn Asn Ala Ala Phe Asp Asp Gly Asp Ser Asn Leu Thr Ser
20 25 30

Ala Ile Glu Ala Ser Trp Ser Ser Asn Leu Asn Ala Ser Phe Asp Ser Asp

35

40

45

Cys Ser Lys Glu Asn Gln Ile Pro Val Ser Val Ser Ser Ser Leu Lys
50 55 60

Ser Ser Val Ser Phe Ser Thr Asp Asp Pro Ile Arg Cys Gly Lys Val
65 70 75 80

Lys Glu Lys Pro His Lys Thr Gly Lys Val Arg His Gly Asp Ile Asp
85 90 95

Ala Glu Ile Glu Glu Val Glu Lys Glu Met Asn Arg Leu Ser Ile Arg
100 105 110

Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Ile Ala
115 120 125

<210> 25

<211> 86

<212> PRT

<213> *Eschscholzia californica*

<400> 25

Met Leu Glu Ile Ser Glu Thr Leu Asn Leu Pro Asp Leu Gln Thr Trp
1 5 10 15

Asn Asn Ala Ala Phe Asp Ser Gly Ser Thr Asp Asn His Thr Thr Ala
20 25 30

Ile Lys Ala Ser Ser Ser Pro Leu Lys Pro Ile Val Leu Asn Gln Ser
35 40 45

Glu Pro Ser Ile Leu Asp Ser Ile Tyr Thr Lys Glu Asn Gln Thr Pro
50 55 60

Ser Cys Cys Ile Ser Pro Val Arg Thr Lys Ser Pro Leu Pro Ile Lys
65 70 75 80

Pro Leu His Pro Asn Gly
85

<210> 26

<211> 144

<212> PRT

<213> *Gossypium arboreum*

<400> 26

Met Ser Ile Leu Gln Tyr Pro Asp Ser Phe Asn Val Pro Glu Leu Gln
 1 5 10 15
 Val Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Thr Asn
 20 25 30
 Ala Ile Lys Asp Ser Trp Cys Asn Phe Asn Ser Gly Ser Val Asn Gln
 35 40 45
 Ser Leu Glu Ser Asp Gly Ser Lys Glu Asn Gln Ser Pro Leu Trp Ile
 50 55 60
 Lys Ser Pro Val Ser Phe Lys Ser Thr Ala Ser Val Val Lys Pro Leu
 65 70 75 80
 Ser Ser Lys Asn Val Thr Gly Asn Thr Arg Glu Pro Phe Ser Ala Lys
 85 90 95
 Met Lys Ser Gly Val Cys Lys Glu Glu Glu Lys Lys Arg Asp Glu Lys
 100 105 110
 Lys Ile Asp Met Glu Ile Glu Glu Ile Glu Lys Glu Val Ala Arg Leu
 115 120 125
 Ser Ala Lys Leu Glu Ser Leu Arg Leu Glu Lys Pro Asn Ile Met Gln
 130 135 140
 <210> 27
 <211> 75
 <212> PRT
 <213> Populus tremula
 <400> 27
 Met Ser Ser Ile Leu Gln Tyr Pro Asp Val Val Asp Ala Pro Glu Val
 1 5 10 15
 Gln Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Glu Ser Glu Gly Ser
 20 25 30
 Leu Asn Leu Lys Ser Ser Trp Trp Asn Gln Ser Leu Glu Ser Asp Ala
 35 40 45
 Ser Lys Glu Asn Leu Ser Pro Val Cys Glu Gln Ser Ser Pro Val Phe
 50 55 60
 Val Asn Ser Ser Lys Pro Ala Lys Pro Leu Gln

65

70

75

<210> 28

<211> 77

<212> PRT

<213> *Plumbao zeylanica*

<400> 28

Met Asn Glu Val Leu His Leu Gln Glu Ala Ala Arg Thr Asp Ser Ser
 1 5 10 15

Thr Asp His Gln Ile Trp Asn Asn Ala Ala Phe Asp Ser Gly Glu Ser
 20 25 30

Glu Asp Ser Pro Val Val Ile Asp Phe Ser Ala Pro Asn Leu Ser Gln
 35 40 45

Ser Leu Leu Ser Asp Ser Ser Ile Lys Glu Asn Leu Ser Pro Ser Leu
 50 55 60

Ala Glu Met Pro His Pro Ala Lys Ser Pro Met Gln Lys
 65 70 75

<210> 29

<211> 139

<212> PRT

<213> *Citrus sinensis*

<400> 29

Met Ser Val Leu Gln Tyr Pro Asp Thr Leu Asn Gly Gln Glu Leu Gln
 1 5 10 15

Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Glu Ser Glu Asp Ser Thr
 20 25 30

Ala Met Lys Gly Ser Trp Ala Asn Leu Lys Ser Val Tyr Met Asn Gln
 35 40 45

Ser Leu Glu Ser Asp Cys Ser Lys Glu Asn Leu Ser Pro Arg Leu Asn
 50 55 60

Lys Ser Pro Thr Ser Ser Leu Lys Ser Cys Val Pro Asn Lys Pro Leu
 65 70 75 80

Gln Val Asn Ser Ser Val Lys Asn Ser Gln Met Lys Gln Leu Lys Ser
 85 90 95

Val Ser Lys Glu Glu Glu Thr Arg Asp Glu Arg Lys Ile Asp Ile Glu
 100 105 110

Ile Glu Glu Ile Glu Lys Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu
 115 120 125

Ala Leu Arg Leu Glu Lys Ile Asp Ile Lys Thr
 130 135

<210> 30
 <211> 186
 <212> PRT
 <213> Hordeum vulgare

<400> 30
 Ile Ser Thr Ala Ser Thr Cys Arg Arg Pro Ala Gly Ser Ser Lys Val
 1 5 10 15

Arg Val Val Pro Ser Arg Tyr Ser Leu Met Pro Gly Ala Ser Leu Gly
 20 25 30

Ala Ala Thr Gln Asp Gly Arg Arg Lys Glu Ser Leu Pro Gly Ser Thr
 35 40 45

Gly Ser Thr Gly Gln Lys Glu Glu Ile Lys Ala Val Pro Thr Glu Pro
 50 55 60

Val Asp Asp Asp Leu Ser Pro Glu Ser Leu Asp Lys Val Ala Glu Leu
 65 70 75 80

Leu Pro Arg Ile Arg Thr Met Pro Arg Pro Asn Glu Thr Pro Pro Asp
 85 90 95

Ser Gly Cys Ala Lys Arg Ala Ala Asp Leu Val Gly Lys Arg Ser Phe
 100 105 110

Phe Ala Ala Ala Ala Ala Gly Asp Gly Ser Ala Ile Ser Ser Tyr Gln
 115 120 125

Ala Arg Val Leu Glu Ala Glu Ala Pro Glu Glu Ala Ala Ala Ala Gly
 130 135 140

Ala Leu Ser Asp Glu Ala Ala Ala Ala Gly Ala Leu Ser Asp Glu Ala
 145 150 155 160

Ala Ala Ala Ala Ala Ala Ala Glu Ala Leu Ser Asp Glu Ala Ala Ala

165

170

175

Ala Glu Ala Leu Ser Asp Glu Ala Ala Ala
180 185

<210> 31

<211> 145

<212> PRT

<213> *Triticum aestivum*

<400> 31

Gly Arg Tyr Ser Leu Met Pro Gly Ala Ser Leu Gly Ala Ala Ser Gln
1 5 10 15

Glu Arg Arg Arg Lys Glu Ser Leu Pro Gly Ser Thr Gly Gly Ala Gly
20 25 30

Gln Lys Glu Glu Glu Ile Lys Ala Met Pro Thr Glu Pro Val Asp Asp
35 40 45

Asp Leu Ser Pro Glu Ser Leu Asp Lys Val Ala Glu Leu Leu Pro Arg
50 55 60

Thr Arg Thr Met Pro Pro Pro Asp Glu Thr Pro Arg Asp Ser Gly Cys
65 70 75 80

Ala Lys Arg Ala Ala Asp Leu Val Gly Lys Arg Ser Phe Phe Ala Ala
85 90 95

Ala Ala Ala Gly Asp Cys Ser Ala Ile Ser Ser Tyr Gln Ala Arg Val
100 105 110

Leu Glu Ala Glu Ala Pro Glu Glu Ala Ala Ala Ala Glu Ala Leu
115 120 125

Gly Asp Glu Ala Ala Ser Ala Gly Glu Ala Leu Gly Asp Glu Ala Ala
130 135 140

Ala

145

<210> 32

<211> 139

<212> PRT

<213> *Zea mays*

<400> 32

Thr Ser Asn Val Ala Thr Thr Lys Arg Pro Ala Gly Ser Ser Lys Val
1 5 10 15

Arg Val Val Pro Ser Arg Tyr Ser Ile Pro Pro Gly Ser Ser Leu Ala
20 25 30

Ala Val Thr Gln Gly Asn Arg Cys Lys Gln Ser Leu Pro Gly Ser Ala
35 40 45

Thr Glu Thr Arg Val Asn Leu Thr Glu Pro Pro Asn Asp Glu Leu Ser
50 55 60

Pro Glu Glu Leu Ala Lys Val Ala Glu Leu Leu Pro Arg Ile Arg Thr
65 70 75 80

Met Pro Pro Ser Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg
85 90 95

Val Ala Asp Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Gly Asp
100 105 110

Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala Arg Val Val Glu Leu Glu
115 120 125

Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu Ala
130 135

<210> 33
<211> 133
<212> PRT
<213> Saccharum sp.

<220>
<221> MOD_RES
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Thr Ser Asn Ala Ala Thr Ala Lys Arg Pro Ala Gly Ser Ser Lys Val
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Arg Val Val Pro Ser Arg Tyr Ser Ile Thr Pro Gly Ser Tyr Leu Ala
20 25 30

Ala Val Ser Gln Asp Lys Arg Ser Lys Gln Ser Leu Pro Gly Pro Ala
35 40 45

Ser Ala Ala Ser Gln Arg Glu Glu Ile Arg Ala Lys Leu Thr Glu Pro
50 55 60

Ser Lys Asp Glu Leu Ser Pro Glu Thr Val Ala Lys Val Ala Glu Leu
65 70 75 80

Leu Pro Arg Ile Lys Thr Met Pro Ala Ser Asp Glu Ser Pro Arg Asp
85 90 95

Ser Ser Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe
100 105 110

Phe Thr Xaa Ala Ala Glu Asp Gly Asn Phe Val Thr Pro Tyr Gln Ala
115 120 125

Pro Val Gly Glu Leu
130

<210> 34
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<213> Pinus taeda

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Xaa Glu Ala Arg Ile Val Phe Gly Thr Gly Asn Ser Ala Ile Met Ala
1 5 10 15

Gly Gly Thr Lys Ala Pro Asp Thr Leu Glu Arg His Lys Met Lys Leu
20 25 30

Pro Lys Ile Lys Thr Val Arg Phe Thr Thr Glu Ser Pro Arg Asp Ser
35 40 45

Gly Cys Ile Lys Arg Glu Ile Asp Arg Ile Gly Lys Lys Ser Phe Phe
50 55 60

Ala Pro Asp Gly Ile Thr Ser Thr Pro Ser Ile Asp Xaa Xaa Asp Ala
65 70 75 80

Gly Lys Pro Leu Arg Arg Glu Ser Val His Glu Ile Xaa His Ala Xaa
85 90 95

Xaa Xaa

<210> 35
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<220>
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Motif 1 CORE peptide

<220>
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Trp Xaa Asn Ala Xaa Xaa Asp
1 5

<210> 36
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<220>
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Motif 3 (coiled core) CORE peptide

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<223> Any amino acid and this region may encompass 1 to 6 residues

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<221> MOD_RES

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<223> Any amino acid

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<223> Any amino acid

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<222> (17)..(18)

<223> Any amino acid

<400> 36

Glu Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Arg Leu Xaa Xaa Xaa Leu

1

5

10

15

Xaa Xaa Leu Arg

20

<210> 37

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Motif 4 CORE peptide

<220>

<221> MOD_RES

<222> (3)..(3)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (5)..(14)

<223> Any amino acid and this region may encompass 1 to 10 residues

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<221> MOD_RES

<222> (19)..(20)

<223> Any amino acid

<220>

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<222> (23)..(28)

<223> Any amino acid and this region may encompass 1 to 6 residues

<400> 37

Leu Pro Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Asp
1 5 10 15

Ser Gly Xaa Xaa Lys Arg Xaa Xaa Xaa Xaa Xaa Xaa Lys
20 25